Amendments to the Specification

Please amend the paragraph bridging pages 13 and 14 as follows:

Two ORFs (SLR0089 and SLR0095) were identified as possible candidates for *Synechocystis* tocopherol methyltransferase genes. BLAST searches with ORFs SLR0089 and SLR0095 showed that these proteins share a high degree of similarity to the known protein sequences of Δ-(24)-sterol-C-methyltransferases and various plant caffeol CoA-O-methyltransferases, respectively. Both SLR0089 and SLR0095 proteins contain consensus sequences corresponding to conserved S-adenosylmethionine (SAM) binding domains (Kagan and Clarke, Archives of Biochem. and Biophy. ~~310(2): 417-427, 1996)~~ 310(2):417-427, 1994).The SLR0089 protein contains other structural features that are consistent with features found in a tocopherol methyltransferase. These features were not found in SLR0095. First, PSORT (Prediction of Protein Localization Sites) computer analysis of the two protein sequences predict that SLR0089 is localized to the plasma membrane, whereas and SLR0095 is localized to the cytosol. Tocopherol biosynthesis in cyanobacteria is believed to occur in the plasma membrane; therefore, localization of SLR0089 protein to the plasma membrane suggests that it may be a tocopherol methyltransferase. Additionally, PSORT analysis identified the presence of a putative bacterial signal sequence in the first 25 amino acids of the SLR0089 protein. The predicted molecular weight of the mature SLR0089 protein (after truncation of the signal sequence) is 32,766 daltons, which is very close to the reported molecular weight (33,000 daltons) of tocopherol methyltransferase purified from pepper fruits (d'Harlingue and Camara, *supra* 1985). The predicted molecular weight of SLR0095 is 24,322 daltons. Therefore, we concluded that of the two identified ORFs, the SLR0089 gene was more likely to be a tocopherol methyltransferase.

Please amend the first full paragraph on page 18 as follows:

The 165H5T7 cDNA may be engineered to contain an *Nco1* site at the transit peptide cleavage site predicted by PSORT using PCR mutagenesis, which would change the amino acid Val-48 to Met. The cDNA ~~will~~ will be ligated to the unique *Nco1* site in the SLR0089 gene replacement plasmid to create an in-frame, amino-terminal fusion between the *Synechoeystis* γ-TMT signal peptide and the plant protein sequence. The construct will be used to transform wild type *Synechoeystis*; transformants will be identified by kanamycin selection. After several single colony passages under selection, gene replacement will be confirmed by PCR. The tocopherol profile of transformants will be determined by HPLC. *Synechoeystis* transformants functionally expressing *Arabidopsis* γ-TMT genes will be identified by their ability to synthesize α-tocopherol in the absence of a functional *Synechoeystis* γ-TMT gene.